

#8



IFWP

RAW SEQUENCE LISTING

DATE: 07/20/2006

PATENT APPLICATION: US/10/533,037

TIME: 19:15:29

Input Set : N:\Crf4\Refhold\10_folder\J533037.raw

Output Set: N:\CRF4\07202006\J533037.raw

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1 <110> APPLICANT: Chang, Chawnshang
2   Yi-Fen Lee
3   Wen-Jye Lin
4 <120> TITLE OF INVENTION: Hydroxyflutamide Induced Pathways
5   Related to Androgen Receptor Negative Prostate Cancer Cells
6 <130> FILE REFERENCE: 21108.0017U2
7 <140> CURRENT APPLICATION NUMBER: US/10/533,037
8 <141> CURRENT FILING DATE: 2005-04-28
9 <150> PRIOR APPLICATION NUMBER: PCT/US03/34636
10 <151> PRIOR FILING DATE: 2003-10-31
11 <150> PRIOR APPLICATION NUMBER: 60/423,340
12 <151> PRIOR FILING DATE: 2002-10-31
13 <160> NUMBER OF SEQ ID NOS: 28
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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17 <211> LENGTH: 1587
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
20 <220> FEATURE:
21 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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25   actgggggaa aaatcacttt ccagtctgtt ttgcaagggtg tgcatttcca tcttgattcc      120
26   ctgaaagtcc atctgtgtgca tcggtcaaga gaaactccac ttgcatgaag attgcacgcc      180
27   tgcagcttgc atctttgttg caaaactagc tacagaagag aagcaaggca aagtcttttg      240
28   tgctcccctc ccccatcaaa ggaaagggga aaatgtctca gtcgaaaggc aagaagcgaa      300
29   accctggcct taaaattcca aaagaagcat ttgaacaacc tcagaccagt tccacaccac      360
30   ctagagattt agactccaag gcttgcatth ctattggaaa tcagaacttt gaggtgaagg      420
31   cagatgacct ggagcctata atggaactgg gacgagggtg gtacggggtg gtggagaaga      480
32   tgcggcacgt gcccagcggg cagatcatgg cagtgaagcg gatccgagcc acagtaaata      540
33   gccaggaaca gaaacgggta ctgatggatt tggatatthc catgaggacg gtggactgtc      600
34   cattcactgt cactttttat ggcgcactgt ttcggggagg tgatgtgtgg atctgcatgg      660
35   agtcatgga tacatcacta gataaattct acaacaagat tattgataaa ggccagacaa      720
36   ttccagagga catcttaggg aaaatagcag tttctattgt aaaagcatta gaacatttac      780
37   atagtaagct gtctgtcatt cacagagacg tcaagccttc taatgtactc atcaatgttc      840
38   tcggtcaagt gaagatgtgc gattttggaa tcagtggcta cttggtggac tctgttgcta      900
39   aaacaattga tgcaggttgc aaaccataca tggccctga aagaataaac ccagagctca      960
40   accagaaggg atacagtgtg aagtctgaca tttggagtct gggcatcacg atgattgagt      1020
41   tggccatcct tcgatttccc tatgattcat ggggaactcc atttcagcag ctcaaacagg      1080
42   tggtagagga gccatcgcca caactcccag cagacaagtt ctctgcagag tttgttgact      1140
43   ttacctcaca gtgtctaaag aagaattcca aagaacggcc tacataccca gagctaattgc      1200
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45      tgattcttgg agactaaaaa gcagtggact taatcgggtg accctactgt ggattgggtg      1320
46      gtttcggggg gaagcaagtt cactacagca tcaatagaaa gtcactcttg agataattta      1380
47      accctgcctc tcagagggtt ttctctccca atttctcttt tactccccct cttaaggggg      1440
48      ccttgaatc tatagtatag aatgaactgt ctagatggat gaattatgat aaaggcttag      1500
49      gacttcaaaa ggtgattaaa tatttaaatga tgtgtcatat gaaaaaaaaa aaaaaaaaaa      1560
50      aaaaaaaaaa aaaaaaaaaa aaaaaaa      1587
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56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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62      Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg Asp
63      20          25          30
64      Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
65      35          40          45
66      Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
67      50          55          60
68      Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
69      65          70          75          80
70      Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
71      85          90          95
72      Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
73      100         105         110
74      Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
75      115         120         125
76      Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
77      130         135         140
78      Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val
79      145         150         155         160
80      Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile
81      165         170         175
82      His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln
83      180         185         190
84      Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val
85      195         200         205
86      Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg
87      210         215         220
88      Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile
89      225         230         235         240
90      Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro
91      245         250         255
92      Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu
93      260         265         270
94      Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val

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95          275          280          285
96  Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr
97          290          295          300
98  Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys
99          305          310          315          320
100  Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp
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106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
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112  agccagccca ttgacatccc agatgccaag aagagaggcc ggaaaaagaa gcgctgtcgg 120
113  gctactgaca gcttctcagg caggttcgaa gatgtctatc agctgcagga ggatgtgctg 180
114  ggggaagggtg ctcacgctcg tgtgcagacc tgtgtcaatc tcatcaccaa ccaggaatat 240
115  gctgtcaaga tcattgagaa gcagctgggc cacatccgca gcagggtgtt ccgggagggtg 300
116  gagatgctgt accagtgccca gggacatagg aatgttctag aactgattga gttctttgag 360
117  gaggaggacc gtttctacct ggtgtttgag aagatgcgtg gcggatccat cctaagccac 420
118  atccatagaa ggcgccactt taacgagctg gaggccagcg tggtagtaca ggacgtggcc 480
119  agtgccctgg acttcctgca taacaaaggc atcgcccaca gggacctaaa gccagagaac 540
120  atcctatgtg agcaccctaa ccaggtctcg ccagtgaaga tctgcgactt cgacctgggc 600
121  agtgggtatca aactcaatgg agactgtccc cccatctcca caccagagct gctcaccctg 660
122  tgtgggtcag ctgagtacat ggcccagag gtggtggagg ccttcagtga agaggccagc 720
123  atctacgaca agcgtcgcga cctgtggagc ctgggcgtca tctctacat cctgcttagt 780
124  ggctaccgcg ccttcgtggg ccactgtggc agcgactgtg gctgggaccg tggggaggcc 840
125  tgtcctgcct gccagaacat gctgtttgag agcatccagg agggcaagta tgagttccct 900
126  gacaaggact ggtcccacat ctcctttgct gccaaagacc tcatctccaa gctgctggtc 960
127  cgagatgccca agcagaggct gagtgtgtgc caagtccctg agcatccctg ggtgcagggg 1020
128  tgtgccccag agaaccacct accgacacct ttggttctgc agaggaacag ctgtgccaaa 1080
129  gacctcacgt cctttgcggc tgaggccatc gccatgaacc ggcagctggc ccagtgtgag 1140
130  gaggacgctg ggcaggacca gcctgtggtc atccgagcta cctcacgctg cctgcagctg 1200
131  tccccacctt cccagtccaa gctggcccag cggcgccaga gggctagcct gtcggccacc 1260
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135  gtccctcccc tgccctgccc acttggtttt gttttgtttg tttttctttg ccgctattga 1500
136  aagcaagtgc ccggaggagg gcgaggggct caggccgccc agcctgcacc ccacgatgct 1560
137  cacctgccaa ctgtgaaggt cctgccacct gcgccccac ctccactcca gccactctgc 1620
138  tgtcttccag ggttggggat cccgcagggt cagcacccca cactctctcc agccctcagt 1680
139  gttgtcaggg acaggccctc ctggtgagca cagtgggtgt tgcattctct caccagagca 1740
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141  tggatgggga cagtgcactt gattgacccc gagtccccat catccacctg cagtgtccct 1860
142  tggagggttg acaatcagaa accctccca ggtgcttag ctccctgccc tgggacagac 1920
143  ctactgtccc caacccact tcccaggggc agagctggaa ggggaccctg caccagcta 1980
144  gctccaccac agcaggagag gtgctggacc aggtttcat cagcaaacat ggggctccca 2040

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145 catgtctccc caccagggc acctgagtgc cccttctcag ggctcagcct gaccacggcc 2100
146 acgtcctgcc cctgggggttc ctaagctctc ctagtctgct ctgttagcca gagctgaggc 2160
147 cataccagg gctctcacct tcctgttgcc cccagagggc agcagctcag gcgtgcctgc 2220
148 tttcaggaaa gggaggctgg gaagggatgt ggtggccctg cggtgcccag acctaaactgc 2280
149 ccgaggcctg tagactgttc tagccgaact actatgcaat acaagtcccc attttctcca 2340
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151 ggtgtctaca gggcagcccc tggcctcaaa aatccttggc caggattgtt tgcagagttt 2460
152 agtttaggct tttttttttt ttttaagaaa ataatttgac ttgcttcctt gttcttgaag 2520
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155 ctgccccacc tgctctgtg gacacatttc caaagaacct ctgggggtgg gacctcctcc 2700
156 atcagtatga ctacagtgtt ggccacctga ggactcggcc cccctgcagg ttctgaagc 2760
157 aacctgactg ggcagtgagc agcattgacc cccactcacc cccaaaacag ggctgtgatt 2820
158 tccttagtcc ttccaagccc gacctggagg atgggtcaga ccccttaact gtgaatgaga 2880
159 catgatcctg ggtgggttc gccacaaacc atgcagaaat ctaaaaggcc tgttgtagag 2940
160 tgggggacat gcaagcactt ttaactccat cgtaccaggt gaactgacct ccggactcct 3000
161 ttcccaccaa ctgtcaacgc caggattttg tattctgttt tgtaaggatt taataaaagt 3060
162 catttaaaaa aaaaaaaaaa 3080
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 412
166 <212> TYPE: PRT
167 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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171 <400> SEQUENCE: 4
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174 Arg Lys Lys Lys Arg Cys Arg Ala Thr Asp Ser Phe Ser Gly Arg Phe
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176 Glu Asp Val Tyr Gln Leu Gln Glu Asp Val Leu Gly Glu Gly Ala His
177 35 40 45
178 Ala Arg Val Gln Thr Cys Val Asn Leu Ile Thr Asn Gln Glu Tyr Ala
179 50 55 60
180 Val Lys Ile Ile Glu Lys Gln Leu Gly His Ile Arg Ser Arg Val Phe
181 65 70 75 80
182 Arg Glu Val Glu Met Leu Tyr Gln Cys Gln Gly His Arg Asn Val Leu
183 85 90 95
184 Glu Leu Ile Glu Phe Phe Glu Glu Glu Asp Arg Phe Tyr Leu Val Phe
185 100 105 110
186 Glu Lys Met Arg Gly Gly Ser Ile Leu Ser His Ile His Arg Arg Arg
187 115 120 125
188 His Phe Asn Glu Leu Glu Ala Ser Val Val Val Gln Asp Val Ala Ser
189 130 135 140
190 Ala Leu Asp Phe Leu His Asn Lys Gly Ile Ala His Arg Asp Leu Lys
191 145 150 155 160
192 Pro Glu Asn Ile Leu Cys Glu His Pro Asn Gln Val Ser Pro Val Lys
193 165 170 175
194 Ile Cys Asp Phe Asp Leu Gly Ser Gly Ile Lys Leu Asn Gly Asp Cys

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195                               180                               185                               190
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199                               210                               215                               220
200 Tyr Asp Lys Arg Cys Asp Leu Trp Ser Leu Gly Val Ile Leu Tyr Ile
201                               225                               230                               235                               240
202 Leu Leu Ser Gly Tyr Pro Pro Phe Val Gly His Cys Gly Ser Asp Cys
203                               245                               250                               255
204 Gly Trp Asp Arg Gly Glu Ala Cys Pro Ala Cys Gln Asn Met Leu Phe
205                               260                               265                               270
206 Glu Ser Ile Gln Glu Gly Lys Tyr Glu Phe Pro Asp Lys Asp Trp Ser
207                               275                               280                               285
208 His Ile Ser Phe Ala Ala Lys Asp Leu Ile Ser Lys Leu Leu Val Arg
209                               290                               295                               300
210 Asp Ala Lys Gln Arg Leu Ser Ala Ala Gln Val Leu Gln His Pro Trp
211                               305                               310                               315                               320
212 Val Gln Gly Cys Ala Pro Glu Asn Thr Leu Pro Thr Pro Leu Val Leu
213                               325                               330                               335
214 Gln Arg Asn Ser Cys Ala Lys Asp Leu Thr Ser Phe Ala Ala Glu Ala
215                               340                               345                               350
216 Ile Ala Met Asn Arg Gln Leu Ala Gln Cys Glu Glu Asp Ala Gly Gln
217                               355                               360                               365
218 Asp Gln Pro Val Val Ile Arg Ala Thr Ser Arg Cys Leu Gln Leu Ser
219                               370                               375                               380
220 Pro Pro Ser Gln Ser Lys Leu Ala Gln Arg Arg Gln Arg Ala Ser Leu
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235 cttcttgctc agtgccctga agtttctctg caatgaactg acaaatcgga accatggtgc 180
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